

9301-237-228 Seqlist.txt

SEQUENCE LISTING

<110> Schadt, Eric E.  
Monks, Stephanie A.

<120> COMPUTER SYSTEMS AND METHODS FOR  
INFERRING CASUALITY FROM CELLULAR CONSTITUENT ABUNDANCE DATA

<130> 9301-237-228

<140> PCT/US2004/017754

<141> 2004-06-04

<150> To be Assigned

<151> 2004-05-28

<150> 60/497,470

<151> 2003-08-21

<150> 60/492,682

<151> 2003-08-05

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 572

<212> PRT

<213> homo sapiens polypeptide

<220>

<223> malic enzyme ME1

<400> 1

Met	Glu	Pro	Glu	Ala	Pro	Arg	Arg	Arg	His	Thr	His	Gln	Arg	Gly	Tyr
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Leu	Leu	Thr	Arg	Asn	Pro	His	Leu	Asn	Lys	Asp	Leu	Ala	Phe	Thr	Leu
			20					25					30		
Glu	Glu	Arg	Gln	Gln	Leu	Asn	Ile	His	Gly	Leu	Leu	Pro	Pro	Ser	Phe
		35				40					45				
Asn	Ser	Gln	Glu	Ile	Gln	Val	Leu	Arg	Val	Val	Lys	Asn	Phe	Glu	His
	50				55						60				
Leu	Asn	Ser	Asp	Phe	Asp	Arg	Tyr	Leu	Leu	Leu	Met	Asp	Leu	Gln	Asp
65				70					75					80	
Arg	Asn	Glu	Lys	Leu	Phe	Tyr	Arg	Val	Leu	Thr	Ser	Asp	Ile	Glu	Lys
			85					90						95	
Phe	Met	Pro	Ile	Val	Tyr	Thr	Pro	Thr	Val	Gly	Leu	Ala	Cys	Gln	Gln
			100				105						110		
Tyr	Ser	Leu	Val	Phe	Arg	Lys	Pro	Arg	Gly	Leu	Phe	Ile	Thr	Ile	His
	115					120					125				
Asp	Arg	Gly	His	Ile	Ala	Ser	Val	Leu	Asn	Ala	Trp	Pro	Glu	Asp	Val
	130				135					140					
Ile	Lys	Ala	Ile	Val	Val	Thr	Asp	Gly	Glu	Arg	Ile	Leu	Gly	Leu	Gly
145				150					155					160	
Asp	Leu	Gly	Cys	Asn	Gly	Met	Gly	Ile	Pro	Val	Gly	Lys	Leu	Ala	Leu
			165				170						175		
Tyr	Thr	Ala	Cys	Gly	Gly	Met	Asn	Pro	Gln	Glu	Cys	Leu	Pro	Val	Ile
		180					185						190		
Leu	Asp	Val	Gly	Thr	Glu	Asn	Glu	Glu	Leu	Leu	Lys	Asp	Pro	Leu	Tyr
	195					200						205			

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Ile Gly Leu Arg Gln Arg Arg Val Arg Gly Ser Glu Tyr Asp Asp Phe
 210      215      220
Leu Asp Glu Phe Met Glu Ala Val Ser Ser Lys Tyr Gly Met Asn Cys
225      230      235      240
Leu Ile Gln Phe Glu Asp Phe Ala Asn Val Asn Ala Phe Arg Leu Leu
      245      250      255
Asn Lys Tyr Arg Asn Gln Tyr Cys Thr Phe Asn Asp Asp Ile Gln Gly
      260      265      270
Thr Ala Ser Val Ala Val Ala Gly Leu Leu Ala Ala Leu Arg Ile Thr
      275      280      285
Lys Asn Lys Leu Ser Asp Gln Thr Ile Leu Phe Gln Gly Ala Gly Glu
      290      295      300
Ala Ala Leu Gly Ile Ala His Leu Ile Val Met Ala Leu Glu Lys Glu
305      310      315      320
Gly Leu Pro Lys Glu Lys Ala Ile Lys Lys Ile Trp Leu Val Asp Ser
      325      330      335
Lys Gly Leu Ile Val Lys Gly Arg Ala Ser Leu Thr Gln Glu Lys Glu
      340      345      350
Lys Phe Ala His Glu His Glu Glu Met Lys Asn Leu Glu Ala Ile Val
      355      360      365
Gln Glu Ile Lys Pro Thr Ala Leu Ile Gly Val Ala Ala Ile Gly Gly
      370      375      380
Ala Phe Ser Glu Gln Ile Leu Lys Asp Met Ala Ala Phe Asn Glu Arg
385      390      395      400
Pro Ile Ile Phe Ala Leu Ser Asn Pro Thr Ser Lys Ala Glu Cys Ser
      405      410      415
Ala Glu Gln Cys Tyr Lys Ile Thr Lys Gly Arg Ala Ile Phe Ala Ser
      420      425      430
Gly Ser Pro Phe Asp Pro Val Thr Leu Pro Asn Gly Gln Thr Leu Tyr
      435      440      445
Pro Gly Gln Gly Asn Asn Ser Tyr Val Phe Pro Gly Val Ala Leu Gly
      450      455      460
Val Val Ala Cys Gly Leu Arg Gln Ile Thr Asp Asn Ile Phe Leu Thr
465      470      475      480
Thr Ala Glu Val Ile Ala Gln Gln Val Ser Asp Lys His Leu Glu Glu
      485      490      495
Gly Arg Leu Tyr Pro Pro Leu Asn Thr Ile Arg Asp Val Ser Leu Lys
      500      505      510
Ile Ala Glu Lys Ile Val Lys Asp Ala Tyr Gln Glu Lys Thr Ala Thr
      515      520      525
Val Tyr Pro Glu Pro Gln Asn Lys Glu Ala Phe Val Arg Ser Gln Met
      530      535      540
Tyr Ser Thr Asp Tyr Asp Gln Ile Leu Pro Asp Cys Tyr Ser Trp Pro
545      550      555      560
Glu Glu Val Gln Lys Ile Gln Thr Lys Val Asp Gln
      565      570

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<210> 2  
 <211> 572  
 <212> PRT  
 <213> mus musculus polypeptide

<220>  
 <223> Mod1

<400> 2  
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 1 5 10 15  
 Leu Leu Thr Arg Asp Pro His Leu Asn Lys Asp Leu Ala Phe Thr Leu  
 20 25 30  
 Glu Glu Arg Gln Gln Leu Asn Ile His Gly Leu Leu Pro Pro Cys Ile  
 35 40 45  
 Ile Ser Gln Glu Leu Gln Val Leu Arg Ile Ile Lys Asn Phe Glu Arg

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50	55	60
Leu Asn Ser Asp Phe	Asp Arg Tyr Leu Leu	Leu Met Asp Leu Gln Asp
65	70	75
Arg Asn Glu Lys Leu Phe	Tyr Ser Val Leu Met Ser Asp Val Glu Lys	80
85	90	95
Phe Met Pro Ile Val Tyr Thr Pro Thr	Val Gly Leu Ala Cys Gln Gln	100
100	105	110
Tyr Ser Leu Ala Phe Arg Lys Pro Arg Gly Leu Phe Ile Ser Ile His	115	125
115	120	125
Asp Lys Gly His Ile Ala Ser Val Leu Asn Ala Trp Pro Glu Asp Val	130	140
130	135	140
Val Lys Ala Ile Val Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly	145	155
145	150	160
Asp Leu Gly Cys Asn Gly Met Gly Ile Pro Val Gly Lys Leu Ala Leu	155	165
165	170	175
Tyr Thr Ala Cys Gly Gly Val Asn Pro Gln Gln Cys Leu Pro Ile Thr	180	190
180	185	190
Leu Asp Val Gly Thr Glu Asn Glu Glu Leu Leu Lys Asp Pro Leu Tyr	195	205
195	200	205
Ile Gly Leu Arg His Arg Arg Val Arg Gly Pro Glu Tyr Asp Ala Phe	210	220
210	215	220
Leu Asp Glu Phe Met Glu Ala Ala Ser Ser Lys Tyr Gly Met Asn Cys	225	235
225	230	235
Leu Ile Gln Phe Glu Asp Phe Ala Asn Arg Asn Ala Phe Arg Leu Leu	235	245
245	250	255
Asn Lys Tyr Arg Asn Lys Tyr Cys Thr Phe Asn Asp Asp Ile Gln Gly	260	270
260	265	270
Thr Ala Ser Val Ala Val Ala Gly Leu Leu Ala Ala Leu Arg Ile Thr	275	285
275	280	285
Lys Asn Lys Leu Ser Asp Gln Thr Val Leu Phe Gln Gly Ala Gly Glu	290	300
290	295	300
Ala Ala Leu Gly Ile Ala His Leu Val Val Met Ala Met Glu Lys Glu	305	315
305	310	315
Gly Leu Ser Lys Glu Asn Ala Arg Lys Lys Ile Trp Leu Val Asp Ser	315	325
325	330	335
Lys Gly Leu Ile Val Lys Gly Arg Ala Ser Leu Thr Glu Glu Lys Glu	335	345
345	350	350
Val Phe Ala His Glu His Glu Glu Met Lys Asn Leu Glu Ala Ile Val	355	365
355	360	365
Gln Lys Ile Lys Pro Thr Ala Leu Ile Gly Val Ala Ala Ile Gly Gly	370	380
370	375	380
Ala Phe Thr Glu Gln Ile Leu Lys Asp Met Ala Ala Phe Asn Glu Arg	385	395
385	390	395
Pro Ile Ile Phe Ala Leu Ser Ser Pro Thr Ser Lys Ala Glu Cys Ser	405	415
405	410	415
Ala Asp Glu Cys Tyr Lys Val Thr Lys Gly Arg Ala Ile Phe Ala Ser	420	430
420	425	430
Gly Ser Pro Phe Asp Pro Val Thr Leu Pro Asp Gly Arg Thr Leu Phe	435	445
435	440	445
Pro Gly Gln Gly Asn Asn Ser Tyr Val Phe Pro Gly Val Ala Leu Gly	450	460
450	455	460
Val Val Ala Cys Gly Leu Arg His Ile Asp Asp Lys Val Phe Leu Thr	465	475
465	470	475
Thr Arg Glu Val Ile Ser Gln Gln Val Ser Asp Lys His Leu Gln Glu	485	495
485	490	495
Gly Arg Leu Tyr Pro Pro Leu Asn Thr Ile Arg Gly Val Ser Leu Lys	500	510
500	505	510
Ile Ala Val Lys Ile Val Gln Asp Ala Tyr Lys Glu Lys Met Ala Thr	515	525
515	520	525
Val Tyr Pro Glu Pro Gln Asn Lys Glu Glu Phe Val Ser Ser Gln Met	530	540
530	535	540
Tyr Ser Thr Asn Tyr Asp Gln Ile Leu Pro Asp Cys Tyr Pro Trp Pro	545	555
545	550	555
Ala Glu Val Gln Lys Ile Gln Thr Lys Val Asn Gln	555	560
555	560	560

&lt;210&gt; 3

&lt;211&gt; 564

&lt;212&gt; PRT

&lt;213&gt; homo sapiens polypeptide - ME3

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 9, 18, 27, 55, 66, 88, 157, 199, 219, 305, 307, 323, 387, 519

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 3

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Ile Lys Glu Lys Gly Lys Pro Leu Xaa Leu Asn Pro Arg Thr Asn Lys
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20      25      30
Leu Leu Pro Pro Lys Ile Glu Thr Gln Asp Ile Gln Ala Leu Arg Phe
35      40      45
His Arg Asn Leu Lys Lys Xaa Thr Ser Pro Leu Glu Lys Tyr Ile Tyr
50      55      60
Ile Xaa Gly Ile Gln Glu Arg Asn Glu Lys Leu Phe Tyr Arg Ile Leu
65      70      75      80
Gln Asp Asp Ile Glu Ser Leu Xaa Pro Ile Val Tyr Thr Pro Thr Val
85      90      95
Gly Leu Ala Cys Ser Gln Tyr Gly His Ile Phe Arg Arg Pro Lys Gly
100     105     110
Leu Phe Ile Ser Ile Ser Asp Arg Gly His Val Arg Ser Ile Val Asp
115     120     125
Asn Trp Pro Glu Asn His Val Lys Ala Val Val Val Thr Asp Gly Glu
130     135     140
Arg Ile Leu Gly Leu Gly Asp Leu Gly Val Tyr Gly Xaa Gly Ile Pro
145     150     155     160
Val Gly Lys Leu Cys Leu Tyr Thr Ala Cys Ala Gly Ile Arg Pro Asp
165     170     175
Arg Cys Leu Pro Val Cys Ile Asp Val Gly Thr Asp Asn Ile Ala Leu
180     185     190
Leu Lys Asp Pro Phe Tyr Xaa Gly Leu Tyr Gln Lys Arg Asp Arg Thr
195     200     205
Gln Gln Tyr Asp Asp Leu Ile Asp Glu Phe Xaa Lys Ala Ile Thr Asp
210     215     220
Arg Tyr Gly Arg Asn Thr Leu Ile Gln Phe Glu Asp Phe Gly Asn His
225     230     235     240
Asn Ala Phe Arg Phe Leu Arg Lys Tyr Arg Glu Lys Tyr Cys Thr Phe
245     250     255
Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Ala Leu Ala Gly Leu Leu
260     265     270
Ala Ala Gln Lys Val Ile Ser Lys Pro Ile Ser Glu His Lys Ile Leu
275     280     285
Phe Leu Gly Ala Gly Glu Ala Ala Leu Gly Ile Ala Asn Leu Ile Val
290     295     300
Xaa Ser Xaa Val Glu Asn Gly Leu Ser Glu Gln Glu Ala Gln Lys Lys
305     310     315     320
Ile Trp Xaa Phe Asp Lys Tyr Gly Leu Leu Val Lys Gly Arg Lys Ala
325     330     335
Lys Ile Asp Ser Tyr Gln Glu Pro Phe Thr His Ser Ala Pro Glu Ser
340     345     350
Ile Pro Asp Thr Phe Glu Asp Ala Val Asn Ile Leu Lys Pro Ser Thr
355     360     365
Ile Ile Gly Val Ala Gly Ala Gly Arg Leu Phe Thr Pro Asp Val Ile

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370          375          380
Arg Ala Xaa Ala Ser Ile Asn Glu Arg Pro Val Ile Phe Ala Leu Ser
385          390          395          400
Asn Pro Thr Ala Gln Ala Glu Cys Thr Ala Glu Glu Ala Tyr Thr Leu
          405          410          415
Thr Glu Gly Arg Cys Leu Phe Ala Ser Gly Ser Pro Phe Gly Pro Val
          420          425          430
Lys Leu Thr Asp Gly Arg Val Phe Thr Pro Gly Gln Gly Asn Asn Val
          435          440          445
Tyr Ile Phe Pro Gly Val Ala Leu Ala Val Ile Leu Cys Asn Thr Arg
          450          455          460
His Ile Ser Asp Ser Val Phe Leu Glu Ala Ala Lys Ala Leu Thr Ser
          465          470          475          480
Gln Leu Thr Asp Glu Leu Ala Gln Gly Arg Leu Tyr Pro Pro Leu
          485          490          495
Ala Asn Ile Gln Glu Val Ser Ile Asn Ile Ala Ile Lys Val Thr Glu
          500          505          510
Tyr Leu Tyr Ala Asn Lys Xaa Ala Phe Arg Tyr Pro Glu Pro Glu Asp
          515          520          525
Lys Ala Lys Tyr Val Lys Glu Arg Thr Trp Arg Ser Glu Tyr Asp Ser
          530          535          540
Leu Leu Pro Asp Val Tyr Glu Trp Pro Glu Ser Ala Ser Ser Pro Pro
          545          550          555          560
Val Ile Thr Glu

```

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<210> 4
<211> 584
<212> PRT
<213> homo sapiens polypeptdie

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<220>
<223> ME2

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<400> 4
Met Leu Ser Arg Leu Arg Val Val Ser Thr Thr Cys Thr Leu Ala Cys
1          5          10          15
Arg His Leu His Ile Lys Glu Lys Gly Lys Pro Leu Met Leu Asn Pro
          20          25          30
Arg Thr Asn Lys Gly Met Ala Phe Thr Leu Gln Glu Arg Gln Met Leu
          35          40          45
Gly Leu Gln Gly Leu Leu Pro Pro Lys Ile Glu Thr Gln Asp Ile Gln
          50          55          60
Ala Leu Arg Phe His Arg Asn Leu Lys Lys Met Thr Ser Pro Leu Glu
          65          70          75          80
Lys Tyr Ile Tyr Ile Met Gly Ile Gln Glu Arg Asn Glu Lys Leu Phe
          85          90          95
Tyr Arg Ile Leu Gln Asp Asp Ile Glu Ser Leu Met Pro Ile Val Tyr
          100          105          110
Thr Pro Thr Val Gly Leu Ala Cys Ser Gln Tyr Gly His Ile Phe Arg
          115          120          125
Arg Pro Lys Gly Leu Phe Ile Ser Ile Ser Asp Arg Gly His Val Arg
          130          135          140
Ser Ile Val Asp Asn Trp Pro Glu Asn His Val Lys Ala Val Val Val
          145          150          155          160
Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly Asp Leu Gly Val Tyr Gly
          165          170          175
Met Gly Ile Pro Val Gly Lys Leu Cys Leu Tyr Thr Ala Cys Ala Gly
          180          185          190
Ile Arg Pro Asp Arg Cys Leu Pro Val Cys Ile Asp Val Gly Thr Asp
          195          200          205
Asn Ile Ala Leu Leu Lys Asp Pro Phe Tyr Met Gly Leu Tyr Gln Lys
          210          215          220

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## 9301-237-228 Seqlist.txt

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Arg Asp Arg Thr Gln Gln Tyr Asp Asp Leu Ile Asp Glu Phe Met Lys
225                230                235                240
Ala Ile Thr Asp Arg Tyr Gly Arg Asn Thr Leu Ile Gln Phe Glu Asp
                245                250                255
Phe Gly Asn His Asn Ala Phe Arg Phe Leu Arg Lys Tyr Arg Glu Lys
                260                265                270
Tyr Cys Thr Phe Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Ala Leu
                275                280                285
Ala Gly Leu Leu Ala Ala Gln Lys Val Ile Ser Lys Pro Ile Ser Glu
                290                295                300
His Lys Ile Leu Phe Leu Gly Ala Gly Glu Ala Ala Leu Gly Ile Ala
305                310                315                320
Asn Leu Ile Val Met Ser Met Val Glu Asn Gly Leu Ser Glu Gln Glu
                325                330                335
Ala Gln Lys Lys Ile Trp Met Phe Asp Lys Tyr Gly Leu Leu Val Lys
                340                345                350
Gly Arg Lys Ala Lys Ile Asp Ser Tyr Gln Glu Pro Phe Thr His Ser
                355                360                365
Ala Pro Glu Ser Ile Pro Asp Thr Phe Glu Asp Ala Val Asn Ile Leu
                370                375                380
Lys Pro Ser Thr Ile Ile Gly Val Ala Gly Ala Gly Arg Leu Phe Thr
385                390                395                400
Pro Asp Val Ile Arg Ala Met Ala Ser Ile Asn Glu Arg Pro Val Ile
                405                410                415
Phe Ala Leu Ser Asn Pro Thr Ala Gln Ala Glu Cys Thr Ala Glu Glu
                420                425                430
Ala Tyr Thr Leu Thr Glu Gly Arg Cys Leu Phe Ala Ser Gly Ser Pro
                435                440                445
Phe Gly Pro Val Lys Leu Thr Asp Gly Arg Val Phe Thr Pro Gly Gln
                450                455                460
Gly Asn Asn Val Tyr Ile Phe Pro Gly Val Ala Leu Ala Val Ile Leu
465                470                475                480
Cys Asn Thr Arg His Ile Ser Asp Ser Val Phe Leu Glu Ala Ala Lys
                485                490                495
Ala Leu Thr Ser Gln Leu Thr Asp Glu Glu Leu Ala Gln Gly Arg Leu
                500                505                510
Tyr Pro Pro Leu Ala Asn Ile Gln Glu Val Ser Ile Asn Ile Ala Ile
                515                520                525
Lys Val Thr Glu Tyr Leu Tyr Ala Asn Lys Met Ala Phe Arg Tyr Pro
                530                535                540
Glu Pro Glu Asp Lys Ala Lys Tyr Val Lys Glu Arg Thr Trp Arg Ser
545                550                555                560
Glu Tyr Asp Ser Leu Leu Pro Asp Val Tyr Glu Trp Pro Glu Ser Ala
                565                570                575
Ser Ser Pro Pro Val Ile Thr Glu
                580

```

&lt;210&gt; 5

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; homo sapiens polynucleotide

&lt;220&gt;

&lt;223&gt; mitochondrial NADP(+)-dependent malic enzyme 3 (NCBI accession number AY424278)

&lt;400&gt; 5

```

atggccttta cccttgaaga aaggctgcag cttggaatcc acggcctaata cccgccctgc 60
tttctgagcc aggacgtcca gctcctccga atcatgagat attacgagcg gcagcagagt 120
gacctggaca agtacatcat tctcatgaca ctccaagacc gtaacgagaa gctcttctac 180
cgagtgtgta cttcggacgt ggagaagttc atgccaatcg tgtacacgcc taccgtgggg 240
ctagcctgtc agcactatgg cctgactttc cgcaggcccc gtggactgtt catcaccatt 300
catgacaaag gtcattctgc aacaatgctg aattcttggc cagaagacaa tattaaggcc 360

```

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ggcatccctg tgggcaagct ggccctgtac acggcatgag gaggggtgaa cccgcagcag 480
tgcctccctg tgctgctgga cgtcggcacc aacaatgagg agctgctcag agaccctctg 540
tacatcgccc tgaaacacca gcgcgtgcac gggaaggcat acgatgactt gctggatgag 600
ttcatgcagg ctgtgacaga caagtgttga ataaattgcc tcatccaatt tgaagacttc 660
gccaatgcca atgccttccg cctgctcaac aaataccgta acaagtactg catgttcaat 720
gatgacatcc aagatgactt ctccagaggg ccaaagaggt cacaactttt cttcaagtga 780
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<210> 6

<211> 1650

<212> DNA

<213> homo sapiens polynucleotide

<220>

<223> mitochondrial NAD-dependent malic enzyme 2 (NCBI accession number XM\_209967)

<400> 6

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ataaaaagaaa aaggcaagcc acttatgctg aatccaagaa caaacaaggg aatggcattt 120
actttacaag aacgacagat gcttggctct caagggtctt tacctcccca aatacagaca 180
taagatatcc aagccttacg attccataga aacttgaaaa aaatgactag cccttcggaa 240
aactatatct acataatggg aatacaagaa agaaatgata aattgtttta tagaatactg 300
caagatgaca cggagagttt aatgccaaat gcatatacac cgacggttgg tcttgtctgc 360
tcccagtggtg gacacctctt tagaagacct aagggtattt ttatttccat ctcagacaga 420
ggcatgttta gatcaattgt ggataagtgg ccagaaaatc atgttaaggc tgttttagtg 480
actgatggag agagaattct gggcatgga gatctgggtg tctatggaat gggaattcca 540
gtaggaaaaa tttgtttgta tacagtttgt ccaggaatat ggcctgatag atgccttctg 600
gtgtgtattg atgtgggagc tgataatatc gcactcttaa aaggcacatt ttacatgggc 660
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gctattactg acagatatgg ctggaacaca ctccttcagt ttgaagggtt tggacatcat 780
aatgcattca gattcttgag aaaataccaa taaaaatgtt gcactttcaa tgatgatatt 840
caagggacag ctgcagtagc tctaataagg cttcttgcaa cacaaaaagt tactagtata 900
ccaatctccg aacacaaaat cttattcctt ggagcaggag agattactct tagaattgca 960
aatctttagt tattgtctat ggtagaaaat ggctgtcag aagaagaggc acaaaagaaa 1020
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gtgaatataa tgaagacttc aactacaatt ggagtgcag gtgctggccg tcttttctact 1200
cctgatgtaa tcagagccat tggctgtatc aatgaaaggc ctgtaatat tgcattaagt 1260
aatcctacag cacaggcgga gtgcaggagt tgcacggctg gagaagcata tacacttaca 1320
gagggcaaat gtttgtttgc cagtggcagt ccatttgggc cagtgaact cacagatggg 1380
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ttgacaagcc acgtgacgga tgacgcgcta gcccagggga gactttactt accacttgct 1560
aatattcaga aagtttctat taacattgct attaaagtta cagaatacct gtatgcta 1620
aaaatggctt tctcaatacc cagaacctga 1650
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<210> 7

<211> 2212

<212> DNA

<213> homo sapiens polynucleotide

<220>

<223> cytosolic malic enzyme 1

<400> 7

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ccccccgtcg ccgccacacc catcagcgcg gctacctgct gacacggaac cctcacctca 180
acaaggactt ggcctttacc ctggaagaga gacagcaatt gaacattcat ggattgttgc 240
caccttccct caacagtcag gagatccagg ttcttagagt agtaaaaaat ttcgagcatc 300
```

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tgaactctga ctttgacagg tatcttctct taatggatct ccaagataga aatgaaaaac 360
tcttttatag agtgctgaca tctgacattg agaaattcat gcctattgtt tatactccca 420
ctgtgggtct ggcttgccaa caatatagtt tgggtgttcg gaagccaaga ggtctcttta 480
ttactatcca cgatcgaggg catattgctt cagttctcaa tgcattggcca gaagatgtca 540
tcaaggccat tgtggtgact gatggagagc gtattcttgg cttgggagac cttgggtgta 600
atggaatggg catccctgtg ggtaaattgg ctctatatac agcttgcgga gggatgaatc 660
ctcaagaatg tctgcctgtc attctggatg tgggaaccga aaatgaggag ttacttaaag 720
atccactcta cattggacta cggcagagaa gagtaagagg ttctgaatat gatgattttt 780
tggacgaatt catggaggca gtttcttcca agtatggcat gaattgcctt attcagtttg 840
aagattttgc caatgtgaat gcatttcgtc tcctgaacaa gtatcgaaac cagtattgca 900
cattcaatga tgatattcaa ggaacagcat ctggtgcagt tgcaggcttc cttgcagctc 960
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ctgccctagg gattgcacac ctgattgtga tggccttgga aaaagaagg ttacccaaaag 1080
agaaagccat caaaaagata tggctggttg attcaaaagg attaatagtt aagggacgtg 1140
cttcttaac acaagagaaa gagaagtttg cccatgaaca tgaagaaatg aagaacctag 1200
aagccattgt tcaagaaata aaaccaactg cctcatagg agttgctgca attgggtggtg 1260
cattctcaga acaaattctc aaagatatgg ctgccttcaa tgaacggcct attatttttg 1320
ctttgagtaa tccaactagc aaagcagaat gttctgcaga gcagtgtctac aaaataacca 1380
agggacgtgc aatttttgcc agtggcagtc cttttgatcc agtcactctt ccaaattggac 1440
agaccctata tcctggccaa ggcaacaatt cctacgtgtt ccctggagtt gctcttggtg 1500
ttgtggcgtg tggattgagg cagatcacag ataataattt cctcactact gctgaggtta 1560
tagctcagca agtgtcagat aaacacttgg aagagggctg gctttatcct cctttgaata 1620
ccattagaga tgtttctctg aaaattgcag aaaagattgt gaaagatgca taccaagaaa 1680
agacagccac agtttatcct gaaccgcaaa acaagaagc atttgtccgc tcccagatgt 1740
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<223> nucleic acid sequence AI506234

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9301-237-228 Seqlist.txt

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 <213> mus musculus polypeptide  
  
 <220>  
 <223> amino acid sequence gi:28279474

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 35 40 45  
 His Leu Val Ser Leu Gly Tyr Gln Val Ser Lys Pro Glu Val Ile Phe  
 50 55 60  
 Lys Leu Glu Gln Gly Glu Glu Pro Trp Ile Ser Glu Lys Glu Ile Gln  
 65 70 75 80  
 Arg Pro Phe Cys Pro Asp Trp Lys Thr Arg Pro Glu Ser Ser Arg Ser

## 9301-237-228 Seqlist.txt

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 His Thr Thr Ile Gly Asp Ile Trp Asn Val Ala Ile Gln Gly His Gln  
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 130 135 140  
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 145 150 155 160  
 Ser Ser Leu Ser Thr Asp Leu Val Pro Gln Leu Asp Ile Ser Ser Ser  
 165 170 175  
 Ile Arg Pro Ser Asp Cys Lys Thr Phe Gly Asn Asn Leu Glu His Asn  
 180 185 190  
 Ser Glu Leu Val Thr Gln Ser Asn Ile Leu Ala Lys Lys Lys Pro Tyr  
 195 200 205  
 Lys Cys Asp Lys Cys Arg Lys Ser Phe Ile His Arg Ser Ser Leu Asn  
 210 215 220  
 Lys His Glu Lys Ile His Lys Gly Asp Pro Tyr Ser Asn Gly Thr Asp  
 225 230 235 240  
 Gln Gly Ala Gln Ser Gly Arg Lys His His Glu Cys Ala Asp Cys Gly  
 245 250 255  
 Lys Thr Phe Leu Trp Arg Thr Gln Leu Thr Glu His Gln Arg Ile His  
 260 265 270  
 Thr Gly Glu Lys Pro Phe Glu Cys Asn Val Cys Gly Lys Ala Phe Arg  
 275 280 285  
 His Ser Ser Ser Leu Gly Gln His Glu Asn Ala His Thr Gly Glu Lys  
 290 295 300  
 Pro Tyr Gln Cys Ser Leu Cys Gly Lys Ala Phe Gln Arg Ser Ser Ser  
 305 310 315 320  
 Leu Val Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Arg Cys  
 325 330 335  
 Asn Leu Cys Gly Arg Ser Phe Arg His Ser Thr Ser Leu Thr Gln His  
 340 345 350  
 Glu Val Thr His Ser Gly Glu Lys Pro Phe Gln Cys Lys Glu Cys Gly  
 355 360 365  
 Lys Ala Phe Ser Arg Cys Ser Ser Leu Val Gln His Glu Arg Thr His  
 370 375 380  
 Thr Gly Glu Lys Pro Phe Glu Cys Ser Ile Cys Gly Arg Ala Phe Gly  
 385 390 395 400  
 Gln Ser Pro Ser Leu Tyr Lys His Met Arg Ile His Lys Arg Ser Lys  
 405 410 415  
 Pro Tyr Gln Ser Asn Asn Phe Ser Leu Ala Phe Val Pro Asn Thr Pro  
 420 425 430  
 Leu Pro Gln Gly Glu Gly Leu Leu Thr Glu Val Lys Ser Tyr His Cys  
 435 440 445  
 Asn Asp Cys Gly Lys Asp Phe Gly His Ile Thr Asp Phe Ser Glu His  
 450 455 460  
 Gln Arg Leu His Ala Gly Glu Asn Ser Tyr Gly Ser Glu Gln Thr Leu  
 465 470 475 480  
 Leu Gly Gln Gln Ser Leu Ser His Pro Arg Glu Lys Pro Tyr Gln Cys  
 485 490 495  
 Asn Val Cys Gly Lys Ala Phe Lys Arg Ser Thr Ser Phe Ile Glu His  
 500 505 510  
 His Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly  
 515 520 525  
 Glu Ala Phe Ser Arg Leu Ser Ser Leu Thr Gln His Glu Arg Thr His  
 530 535 540  
 Thr Gly Glu Lys Pro Tyr Glu Cys Ile Asp Cys Gly Lys Ala Phe Ser  
 545 550 555 560  
 Gln Ser Ser Ser Leu Ile Gln His Glu Arg Thr His Thr Gly Glu Lys  
 565 570 575  
 Pro Tyr Glu Cys Asn Glu Cys Gly Arg Ala Phe Arg Lys Lys Thr Asn  
 580 585 590  
 Leu His Asp His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Ala Cys

## 9301-237-228 Seqlist.txt

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 Lys Glu Cys Gly Arg Asn Phe Ser Arg Ser Ser Ala Leu Thr Lys His  
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 His Arg Val His Ala Arg Asn Lys Leu Gln Glu Ser  
 625 630 635

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 <213> mus musculus polynucleotide

<220>  
 <223> nucleic acid sequence AY027436

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 aaatctgagt tcctccgtca tttccacacc tccatcttct ccagaagtga acagggaatc 720  
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 <213> mus musculus polynucleotide

<220>  
 <223> nucleic acid sequence NM\_008288

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 ctggttgatg gcagttatga aaaattacct cctcccgatc ctgggtgctc ccctggccta 180  
 ctactactat tctacaaatg aagagttcag accagaaatg ctccaggga agaaagtgat 240  
 tgctactggg gccagcaaag ggattggaag agaaatggca tatcatctgt caaaaatggg 300  
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## 9301-237-228 Seqlist.txt

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1350

&lt;210&gt; 13

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; mus musculus Polypeptide

&lt;220&gt;

&lt;223&gt; amino acid sequence hydroxysteroid 11-beta dehydrogenase

&lt;400&gt; 13

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 35          40          45
Glu Met Ala Tyr His Leu Ser Lys Met Gly Ala His Val Val Leu Thr
 50          55          60
Ala Arg Ser Glu Glu Gly Leu Gln Lys Val Val Ser Arg Cys Leu Glu
 65          70          75          80
Leu Gly Ala Ala Ser Ala His Tyr Ile Ala Gly Thr Met Glu Asp Met
 85          90          95
Thr Phe Ala Glu Gln Phe Ile Val Lys Ala Gly Lys Leu Met Gly Gly
100          105          110
Leu Asp Met Leu Ile Leu Asn His Ile Thr Gln Thr Ser Leu Ser Leu
115          120          125
Phe His Asp Asp Ile His Ser Val Arg Arg Val Met Glu Val Asn Phe
130          135          140
Leu Ser Tyr Val Val Met Ser Thr Ala Ala Leu Pro Met Leu Lys Gln
145          150          155          160
Ser Asn Gly Ser Ile Ala Val Ile Ser Ser Leu Ala Gly Lys Met Thr
165          170          175
Gln Pro Met Ile Ala Pro Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly
180          185          190
Phe Phe Ser Thr Ile Arg Thr Glu Leu Tyr Ile Thr Lys Val Asn Val
195          200          205
Ser Ile Thr Leu Cys Val Leu Gly Leu Ile Asp Thr Glu Thr Ala Met
210          215          220
Lys Glu Ile Ser Gly Ile Ile Asn Ala Gln Ala Ser Pro Lys Glu Glu
225          230          235          240
Cys Ala Leu Glu Ile Ile Lys Gly Thr Ala Leu Arg Lys Ser Glu Val
245          250          255
Tyr Tyr Asp Lys Ser Pro Leu Thr Pro Ile Leu Leu Gly Asn Pro Gly
260          265          270
Arg Lys Ile Met Glu Phe Phe Ser Leu Arg Tyr Tyr Asn Lys Asp Met
275          280          285
Phe Val Ser Asn
290

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&lt;210&gt; 14

&lt;211&gt; 1437

&lt;212&gt; DNA

&lt;213&gt; mus musculus polynucleotide

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for AK004942

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; mus musculus polypeptide

&lt;220&gt;

&lt;223&gt; amino acid sequence for Gpx3

&lt;400&gt; 15

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His Gly Gly Met Ser Gly Thr Ile Tyr Glu Tyr Gly Ala Leu Thr Ile
35     40     45
Asp Gly Glu Glu Tyr Ile Pro Phe Lys Gln Tyr Ala Gly Lys Tyr Ile
50     55     60
Leu Phe Val Asn Val Ala Ser Tyr Gly Leu Thr Asp Gln Tyr Leu Glu
65     70     75     80
Leu Asn Ala Leu Gln Glu Glu Leu Gly Pro Phe Gly Leu Val Ile Leu
85     90     95
Gly Phe Pro Ser Asn Gln Phe Gly Lys Gln Glu Pro Gly Glu Asn Ser
100    105    110
Glu Ile Leu Pro Ser Leu Lys Tyr Val Arg Pro Gly Gly Phe Val
115    120    125
Pro Asn Phe Gln Leu Phe Glu Lys Gly Asp Val Asn Gly Glu Lys Glu
130    135    140
Gln Lys Phe Tyr Thr Phe Leu Lys Asn Ser Cys Pro Pro Thr Ala Glu
145    150    155    160
Leu Leu Gly Ser Pro Gly Arg Leu Phe Trp Glu Pro Met Lys Ile His
165    170    175
Asp Ile Arg Trp Asn Phe Glu Lys Phe Leu Val Gly Pro Asp Gly Ile
180    185    190

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## 9301-237-228 Seqlist.txt

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 Lys  
 225

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 <212> PRT  
 <213> mus musculus polypeptide

<220>  
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## 9301-237-228 Seqlist.txt

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 50 55 60  
 Pro Ile Gln Ser Pro Ala Asp Pro Glu Ala Ser Gly Thr Thr Glu Leu  
 65 70 75 80  
 Ser His Glu Gln Ala Leu Ser Leu Gly Ser Pro His Thr Pro Ala Pro  
 85 90 95  
 Pro Ala Ala Arg Gly Phe Ser Arg Ala Ile Glu Ser Ser Gly Asp Leu  
 100 105 110  
 Leu His Arg Ile Lys Asp Glu Val Gly Ala Pro Gly Ile Val Val Gly  
 115 120 125  
 Val Ser Val Asp Gly Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala  
 130 135 140  
 Asp Val Glu Asn Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile  
 145 150 155 160  
 Ala Ser Ile Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp  
 165 170 175  
 Glu Ala Gly Lys Leu Asp Leu Asp Leu Pro Val Gln His Tyr Val Pro  
 180 185 190  
 Glu Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr  
 195 200 205  
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys Asp  
 210 215 220  
 Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys Met Val  
 225 230 235 240  
 Lys Gly Thr Pro Pro Pro Asp Gln Glu Lys Glu Leu Lys Glu Lys  
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 260 265 270  
 Gln Asp Ser Glu Ala Arg Cys Arg Ser Ala Lys Pro Gly Lys Lys Lys  
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 340 345 350  
 Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln Glu Glu Asn  
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 Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr Lys Trp Ala  
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 420 425 430  
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 Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu Gly Lys Tyr  
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 Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala Val Gly Ala  
 485 490 495  
 Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Ser Glu Ala Val  
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## 9301-237-228 Seqlist.txt

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 Phe Asp Lys Asp Arg Ala Asp  
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<220>  
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<220>  
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 Leu His Leu Gln Lys Thr Thr Val Gln Phe Arg Gly Pro Thr Gln Ser  
 35 40 45  
 Leu Ala Ser Gly Ile Ser Ala Gly Gln Leu Tyr Ser Thr Gln Ala Ala  
 50 55 60  
 Glu Asp Lys Glu Glu Glu Ser Leu His Ser Ile Ile Ser Asn Thr Glu  
 65 70 75 80  
 Ala Val Arg Gly Ser Val Ser Lys His Glu Phe Gln Ala Glu Thr Lys  
 85 90 95  
 Lys Leu Leu Asp Ile Val Ala Arg Ser Leu Tyr Ser Glu Lys Glu Val  
 100 105 110  
 Phe Ile Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Glu Lys Leu  
 115 120 125  
 Arg His Lys Leu Val Cys Glu Gly Gln Val Leu Pro Glu Met Glu Ile  
 130 135 140  
 His Leu Gln Thr Asp Ala Lys Lys Gly Thr Ile Thr Ile Gln Asp Thr  
 145 150 155 160  
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 165 170 175  
 Ala Arg Ser Gly Ser Lys Ala Phe Leu Glu Ala Leu Gln Asn Gln Ala  
 180 185 190  
 Glu Thr Ser Ser Lys Ile Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser  
 195 200 205  
 Ala Phe Met Val Ala Asp Lys Val Glu Val Tyr Ser Arg Ser Ala Ala  
 210 215 220  
 Pro Glu Ser Pro Gly Tyr Gln Trp Leu Ser Asp Gly Ser Gly Val Phe  
 225 230 235 240  
 Glu Ile Ala Glu Ala Ser Gly Val Arg Pro Gly Thr Lys Ile Ile Ile  
 245 250 255  
 His Leu Lys Ser Asp Cys Lys Asp Phe Ala Ser Glu Ser Arg Val Gln  
 260 265 270  
 Asp Val Val Thr Lys Tyr Ser Asn Phe Val Ser Phe Pro Leu Tyr Leu  
 275 280 285  
 Asn Gly Lys Arg Ile Asn Thr Leu Gln Ala Ile Trp Met Met Asp Pro  
 290 295 300  
 Lys Asp Ile Ser Glu Phe Gln His Glu Glu Phe Tyr Arg Tyr Ile Ala  
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 Gln Ala Tyr Asp Lys Pro Arg Phe Thr Leu His Tyr Lys Thr Asp Ala  
 325 330 335  
 Pro Leu Asn Ile Arg Ser Ile Phe Tyr Val Pro Glu Met Lys Pro Ser  
 340 345 350  
 Met Phe Asp Val Ser Arg Glu Leu Gly Ser Ser Val Ala Leu Tyr Ser  
 355 360 365  
 Arg Lys Val Leu Ile Gln Thr Lys Ala Ala Asp Ile Leu Pro Lys Trp  
 370 375 380  
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 385 390 395 400  
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 405 410 415  
 Asp Val Leu Gln Gln Arg Leu Ile Lys Phe Phe Ile Asp Gln Ser Lys  
 420 425 430  
 Lys Asp Ala Glu Lys Tyr Ala Lys Phe Phe Glu Asp Tyr Gly Leu Phe  
 435 440 445  
 Met Arg Glu Gly Ile Val Thr Ala Glu Gln Asp Ile Lys Glu Asp  
 450 455 460  
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## 9301-237-228 Seqlist.txt

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 545 550 555 560  
 Lys Glu Glu Lys Phe Glu Asp Thr Ser Pro Ala Asp Glu Arg Leu Ser  
 565 570 575  
 Glu Lys Glu Thr Glu Asp Leu Met Ala Trp Met Arg Asn Ala Leu Gly  
 580 585 590  
 Ser Arg Val Thr Asn Val Lys Val Thr Phe Arg Leu Asp Thr His Pro  
 595 600 605  
 Ala Met Val Thr Val Leu Glu Met Gly Ala Ala Arg His Phe Leu Arg  
 610 615 620  
 Met Gln Gln Leu Ala Lys Thr Gln Glu Glu Arg Ala Gln Leu Leu Gln  
 625 630 635 640  
 Pro Thr Leu Glu Ile Asn Pro Arg His Thr Leu Ile Lys Lys Leu Cys  
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 Gln Leu Arg Glu Ser Glu Pro Glu Leu Ala Gln Leu Leu Val Asp Gln  
 660 665 670  
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 His  
 705

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&lt;211&gt; 3106

&lt;212&gt; DNA

&lt;213&gt; mus musculus polynucleotide

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for AK004980

&lt;400&gt; 20

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## 9301-237-228 Seqlist.txt

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&lt;210&gt; 21

&lt;211&gt; 2493

&lt;212&gt; DNA

&lt;213&gt; mus musculus polynucleotide

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for NM\_008194

&lt;400&gt; 21

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## 9301-237-228 Seqlist.txt

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&lt;211&gt; 524

&lt;212&gt; PRT

&lt;213&gt; mus musculus Polypeptide

&lt;220&gt;

&lt;223&gt; amino acid sequence for glycerol kinase (Gyk)

&lt;400&gt; 22

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Ala Glu Leu Leu Ser His His Gln Val Glu Ile Lys Gln Glu Phe Pro
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Arg Glu Gly Trp Val Glu Gln Asp Pro Lys Glu Ile Leu Gln Ser Val
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Tyr Glu Cys Ile Glu Lys Thr Cys Glu Lys Leu Gly Gln Leu Asn Ile
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Thr Val Val Trp Asp Lys Val Thr Gly Glu Pro Leu Tyr Asn Ala Val
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Val Trp Leu Asp Leu Arg Thr Gln Ser Thr Val Glu Asn Leu Ser Lys
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Val Lys Lys Val Gln Glu Ala Val Glu Glu Asn Arg Ala Leu Phe Gly
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Thr Ile Asp Ser Trp Leu Ile Trp Ser Leu Thr Gly Gly Ile His Gly
          180         185         190
Gly Val His Cys Thr Asp Val Thr Asn Ala Ser Arg Thr Met Leu Phe
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Asn Ile His Ser Leu Glu Trp Asp Lys Glu Leu Cys Glu Phe Phe Gly
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Ile Pro Met Glu Ile Leu Pro Asn Val Arg Ser Ser Ser Glu Ile Tyr
225         230         235         240
Gly Leu Met Lys Ala Gly Ala Leu Glu Gly Val Pro Ile Ser Gly Cys
          245         250         255
Leu Gly Asp Gln Ser Ala Ala Leu Val Gly Gln Met Cys Phe Gln Asp
          260         265         270
Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Cys Asn
          275         280         285
Thr Gly His Lys Cys Val Phe Ser Glu His Gly Leu Leu Thr Thr Val
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Ala Tyr Lys Leu Gly Arg Asp Lys Pro Val Tyr Tyr Ala Leu Glu Gly

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9301-237-228 Seqlist.txt

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305          310          315          320
Ser Val Ala Ile Ala Gly Ala Val Ile Arg Trp Leu Arg Asp Asn Leu
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Gly Thr Ser Tyr Gly Cys Tyr Phe Val Pro Ala Phe Ser Gly Leu Tyr
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          370          375          380
Gln Phe Thr Asn Lys Cys His Ile Ala Phe Ala Ala Leu Glu Ala Val
385          390          395          400
Cys Phe Gln Thr Arg Glu Ile Leu Asp Ala Met Asn Arg Asp Cys Gly
          405          410          415
Ile Pro Leu Ser His Leu Gln Val Asp Gly Gly Met Thr Ser Asn Lys
          420          425          430
Ile Leu Met Gln Leu Gln Ala Asp Ile Leu Tyr Ile Pro Val Val Lys
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Pro Ser Met Pro Glu Thr Thr Ala Leu Gly Ala Ala Met Ala Ala Gly
          450          455          460
Ala Ala Glu Gly Val Gly Val Trp Ser Leu Glu Pro Glu Asp Leu Ser
465          470          475          480
Ala Val Thr Met Glu Arg Phe Glu Pro Gln Ile Asn Ala Glu Glu Ser
          485          490          495
Glu Ile Arg Tyr Ser Thr Trp Lys Lys Ala Val Met Lys Ser Ile Gly
          500          505          510
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<223> nucleic acid sequence for NM\_008509

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9301-237-228 Seqlist.txt

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Asp Phe Ser Asp Ile Glu Ser Lys Phe Ala Leu Arg Thr Pro Glu Asp
          35          40          45
Thr Ala Glu Asp Thr Cys His Leu Ile Pro Gly Leu Ala Asp Ser Val
          50          55          60
Ser Asn Cys His Phe Asn His Ser Ser Lys Thr Phe Val Val Ile His
          65          70          75          80
Gly Trp Thr Val Thr Gly Met Tyr Glu Ser Trp Val Pro Lys Leu Val
          85          90          95
Ala Ala Leu Tyr Lys Arg Glu Pro Asp Ser Asn Val Ile Val Val Asp

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## 9301-237-228 Seqlist.txt

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 180  
 Glu Ala Pro Ser Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val  
 195  
 Leu His Thr Phe Thr Arg Gly Ser Pro Gly Arg Ser Ile Gly Ile Gln  
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 Lys Pro Val Gly His Val Asp Ile Tyr Pro Asn Gly Gly Thr Phe Gln  
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 Glu Asn Gly Lys Gln His Asn Gln Ala Phe Glu Ile Ser Leu Tyr Gly  
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 385  
 Glu Leu Leu Met Met Lys Leu Lys Trp Met Ser Asp Ser Tyr Phe Ser  
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 Trp Pro Asp Trp Trp Ser Ser Pro Ser Phe Val Ile Glu Arg Ile Arg  
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 450  
 Cys His Asp Lys Ser Leu Lys Lys Ser Gly  
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